

Table S7: Protein disorder abundance for disorder regions > 50 residues.

Organism ^a	"%long50" ^b		
	MD ^c	IUPred ^c	NORSnet ^c
Thermophiles			
<i>Thermosynechococcus elongatus</i> BP-1	5.2 ± 0.6	1.9 ± 0.4	1.8 ± 0.4
<i>Clostridium clariflavum</i> DSM 19732	6.3 ± 0.6	1.7 ± 0.3	0.8 ± 0.2
<i>Streptococcus thermophilus</i> LMG 18311	8 ± 1	2.0 ± 0.7	1.4 ± 0.5
Hyperthermophiles			
<i>Aeropyrum pernix</i> K1	3.2 ± 0.8	0.5 ± 0.3	0.3 ± 0.2
<i>Pyrococcus horikoshii</i> OT3	2.8 ± 0.7	0.3 ± 0.2	1.8 ± 0.5
Psychrophiles			
<i>Desulfotalea psychrophila</i> LSv54	4.7 ± 0.5	1.3 ± 0.3	0.9 ± 0.2
<i>Colwellia psychrerythraea</i> 34H	4.7 ± 0.5	1.4 ± 0.3	0.8 ± 0.2
<i>Shewanella woodyi</i> ATCC 51908	5.2 ± 0.6	1.6 ± 0.3	1.0 ± 0.3
Psychrotolerants			
<i>Methanococcoides burtonii</i> DSM 6242	4.7 ± 0.8	2.2 ± 0.6	0.6 ± 0.3
<i>Leuconostoc citreum</i> KM20	7 ± 1	2.8 ± 0.7	1.1 ± 0.4
<i>Bacillus weihenstephanensis</i> KBAB4	6.5 ± 0.6	2.2 ± 0.4	0.9 ± 0.2
<i>Rhodoferax ferrireducens</i> T118	5.6 ± 0.6	2.4 ± 0.4	1.6 ± 0.3
Halophiles			
<i>Haloarcula marismortui</i> ATCC 43049	10.7 ± 0.9	12.3 ± 0.9	2.6 ± 0.4
<i>Halobacterium</i> sp. NRC-1	9 ± 1	11 ± 1	2.0 ± 0.5
<i>Marinobacter aquaeolei</i> VT8	7.1 ± 0.7	4.3 ± 0.6	1.6 ± 0.4
Alkalophile			
<i>Bacillus halodurans</i> C-125	6.1 ± 0.7	2.3 ± 0.5	0.5 ± 0.2
Radiation resistant			
<i>Deinococcus deserti</i> VCD115	4.7 ± 0.5	4.4 ± 0.5	1.9 ± 0.3
<i>Deinococcus maricopensis</i> DSM 21211	4.6 ± 0.5	4.6 ± 0.5	1.4 ± 0.3
<i>Deinococcus radiodurans</i>	6.3 ± 0.6	6.6 ± 0.6	3.1 ± 0.4
Taxonomic neighbors (mesophiles)			
<i>Caulobacter vibrioides</i>	7.6 ± 0.8	5.2 ± 0.7	3.0 ± 0.5
<i>Chromobacterium violaceum</i> ATCC 12472	6.6 ± 0.7	3.4 ± 0.5	1.9 ± 0.4
<i>Clostridium acetobutylicum</i>	6.0 ± 0.7	1.0 ± 0.3	0.3 ± 0.2
<i>Corynebacterium glutamicum</i>	7.7 ± 0.8	6.4 ± 0.8	2.3 ± 0.5
<i>Desulfovibrio vulgaris</i> str. Hildenborough	7.9 ± 0.8	6.1 ± 0.6	2.3 ± 0.4
<i>Geobacter metallireducens</i> GS-15	6.3 ± 0.8	3.0 ± 0.5	1.5 ± 0.4
<i>Geobacter sulfurreducens</i> PCA	5.9 ± 0.8	3.1 ± 0.6	1.7 ± 0.4
<i>Lactococcus lactis</i> subsp. <i>lactis</i> II1403	8 ± 1	2.3 ± 0.6	1.2 ± 0.4

<i>Listeria innocua</i>	7.2 ± 0.9	2.4 ± 0.5	0.6 ± 0.3
<i>Methanosarcina mazei</i> Go1	6.0 ± 0.7	3.2 ± 0.5	1.4 ± 0.4
<i>Methanococcus maripaludis</i> S2	4.7 ± 0.9	0.9 ± 0.4	0.4 ± 0.3
<i>Nitrosomonas europaea</i> ATCC 19718	5.7 ± 0.9	2.2 ± 0.5	1.1 ± 0.4
<i>Pseudoalteromonas atlantica</i> T6c	5.2 ± 0.6	2.6 ± 0.4	1.1 ± 0.3
<i>Rhodopseudomonas palustris</i> CGA009	7.6 ± 0.7	5.7 ± 0.6	2.9 ± 0.4
<i>Rhodospirillum rubrum</i> ATCC 11170	6.5 ± 0.7	4.4 ± 0.6	2.4 ± 0.4
<i>Rhodobacter sphaeroides</i> 2.4.1	6.7 ± 0.7	4.6 ± 0.6	2.2 ± 0.4
<i>Shewanella oneidensis</i>	6.3 ± 0.6	1.9 ± 0.4	1.0 ± 0.3
<i>Ruegeria pomeroyi</i> DSS-3	4.1 ± 0.6	2.4 ± 0.4	0.9 ± 0.3
<i>Streptomyces coelicolor</i>	9.3 ± 0.6	12.2 ± 0.6	5.2 ± 0.5
<i>Synechococcus elongatus</i> PCC 6301	5.4 ± 0.8	2.4 ± 0.6	2.0 ± 0.5
<i>Synechocystis</i> sp. PCC 6803 substr. Kazusa	6.6 ± 0.8	3.3 ± 0.6	1.8 ± 0.5
Eukaryotes			
<i>Arabidopsis thaliana</i>	27.8 ± 0.5	18.3 ± 0.4	23.5 ± 0.5
<i>Caenorhabditis elegans</i>	27.5 ± 0.5	23.7 ± 0.5	23.0 ± 0.5
<i>Dictyostelium discoideum</i>	34.0 ± 0.8	33.5 ± 0.7	23.2 ± 0.7
<i>Drosophila melanogaster</i>	38.3 ± 0.8	35.4 ± 0.7	33.6 ± 0.7
<i>Schizosaccharomyces pombe</i> 972h-	31 ± 1	20 ± 1	23 ± 1
<i>Saccharomyces cerevisiae</i> S288c	33 ± 1	25 ± 1	24 ± 1

- a. Organism marks the full name of the organism where grey cells correspond to the environments; Taxonomic neighbors correspond to organisms that are related in phylogeny to the extremophiles described in this study. Eukaryotes picked at random from the set of completely sequenced organisms in UniProt.
- b. Disorder %long50 refers to the percentage of proteins in a proteome that contains at least one region with ≥ 50 consecutive residues predicted as disordered.
- c. <MD | IUPred | NORSpnet> refer to the three prediction methods used, in order to catch the different “flavors” of disorder.